Research Note

Evaluation of Bole Straightness in Cottonwood Using Visual Scores

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SUMMARY

Selection for straightness in natural stands of cottonwood can be effective in improving straightness of open-pollinated progeny. Straightness appears to be highly heritable, but it is subject to imprecise evaluation. This can be largely overcome by repeated application of an imprecise scoring system using a minimum of two views per tree separated by 90 degrees.

Additional keywords: Clone, crook, heritability.

INTRODUCTION

Bole straightness is an important character which must be considered in development of genetically improved trees for sawlog and veneer production. However, it is difficult to quantify. Use of subjective techniques is the only practical way to evaluate large numbers of trees (Shelbourne 1966). Done properly, the evaluation of straightness correlates with actual yield of lumber (Miller 1975). In the present study, several scoring observations per tree were made to examine the advantages of multiple observations per tree in a replicated cottonwood clonal test.

MATERIALS AND METHODS

Straightness was scored in a 7-year-old plantation in which tree heights averaged 22 m and diameters at breast height (dbh) averaged 20 cm. The study initially consisted of 80 clones, 5 replications, and 4-tree linear plots at 3×3 m spacing. A randomized-complete-block design was used. Alternate row thinning at age 3 removed two trees per plot. The poorer of the two remaining trees was removed at age 5. One clone was poorly adapted and died. The remaining clones included a select group of 37 clones, a random group of 40 clones and two other clones which did not fit into either group and were eliminated from consideration. The select group averaged 1.5 cm greater diameter than did the random group and consisted of from 1 to 8 cloned open-pollinated progeny from each of 15 female parent trees. Parents had been chosen from natural stands on the basis of phenotypic superiority in a number of characters, including straightness. Progeny were chosen on the basis of fast growth as seedlings and as clones in 1-year tests. The random group consisted of cloned young trees randomly selected from six stands in the general vicinity of the select parents.

A 1 to 9 straightness score was used with 1 being very straight, 9 very crooked, and 5 near the average. Two scorers, A and B, having 3 and 8 years cottonwood research experience, respectively, examined several trees and attempted to standardize their scoring procedure, lumping crook, sweep and lean into a single score. Each then scored the 385 trees 4 times, first from the west, then from the east, north, and south, standing 9 m (3 planting spaces) from the base of the tree and observing approximately the lower 10 m of the tree. Scores were called off to assistants, enabling scorers to devote their full attention to the trees and remaining unaware of clonal identity. The two scorers stayed far enough apart to avoid hearing each other's scores. Rest breaks were scheduled be-

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tween directions of scoring. Scoring each tree from each of 4 sides by each scorer resulted in 8 observations per tree.

Each of the 8 sets of observations was separated into select and random groups. The resulting 16 sets of data and various combinations of sets, consisting of the mean of two or more observations per tree, were subjected to analysis of variance. The limitations of analysis of variance in dealing with subjective "score" data were ignored. Analysis was according to the following form:

Source	df	E(MS)
Replications	$r-1$	$\sigma_e^2 + c\sigma_r^2$
Clones	$c-1$	$\sigma_e^2 + r\sigma_c^2$
Rep × Clone	$(r-1)(c-1)$	σ_e^2

The proportion of variation due to the clonal component (σ_c^2) was then computed. Simple correlations between various observations were also computed.

RESULTS

Clone straightness scores computed over directions and scorers averaged 3.9 for the select group and ranged from 1.7 to 6.5. The random group was significantly more crooked (.05 level), averaging 4.7 and ranging from 2.0 to 7.1.

Scorer B scored the select group 0.2 units more severely and the random group 0.6 units more severely than did scorer A. The difference among scorers was statistically significant at the .05 level in both groups. Scorer B also utilized approximately 1.5 units greater spread in scoring. Both error and clonal components of variance for B's data were greater than for A's data. The proportion of total variation attributable to clones was greater for scorer B than for scorer A, particularly in the select group (table 1). Scorer B's correlations between observations from different directions were consistently about 0.10 higher than those for scorer A (table 2).

A single observation per tree would have been sufficient to detect significant differences among clones within groups. Multiple observations increased the proportion of total variation attributable to clones. On the average, clonal variance computed from a single set of scores represented 37 percent of the total variation, while analysis of the mean of two scores per tree from directions differing by 90 degrees increased this percentage to 53, and averaging the scores from all 4 sides further increased the percentage to 58. Utilization of information from 4 directions from a second scorer further increased clonal variance to 63 percent of the total within-group variance. Clonal variance as a proportion of total variance is equivalent to broad sense heritability on an individual tree basis over the entire area (5 replications) of the experiment ($\sigma_c^2/\sigma_c^2 + \sigma_e^2 + \sigma_r^2$)).

Table 1.—*Proportion of variation in straightness attributable to clones*

Direction	Select		Random	
	A	B	A	B
West	.26	.43	.44	.47
East	.25	.35	.32	.44
North	.25	.35	.34	.42
South	.36	.40	.40	.37
X̄	.28	.38	.38	.43
W + E	.30	.44	.44	.50
N + S	.39	.44	.43	.45
X̄	.34	.44	.43	.47
W + N	.39	.55	.59	.62
E + S	.41	.55	.54	.56
X̄	.40	.55	.56	.59
W + E + N + S	.45	.60	.62	.64
W + E + N + S (Combined over observers)	.58		.68	

Table 2.—*Correlations between directions for straightness*

Direction	Scorer	
	A	B
West with east	.70	.82
North with south	.65	.75
West with north	.35	.46
East with south	.38	.44
W + E with N + S	.45	.50

CONCLUSIONS

Selection in natural stands for straightness appears to be effective, since the clones derived from open-pollinated progeny of phenotypically superior female parent trees averaged nearly one full unit straighter than did the random clones.

Although straightness is highly heritable in cottonwood, imprecise evaluation effectively reduces heritability. This can be overcome by making more than one observation per tree. Apparent straightness depends on the side of the tree viewed. Two 90 degree opposed views substantially improve assessment of straightness. Additional observations make only minor contributions. Precision may differ sufficiently among scorers to justify comparison of samples of their work prior to launching a large-scale effort to score straightness.

LITERATURE CITED

Miller, R.G.
1975. Visual assessment of stem straightness in radiata pine. Aust. For. Res. 7(1):45–56.
Shelbourne, C.J.
1966. Studies on the inheritance and relationship of bole straightness and compression wood in southern pines. Ph.D. Thesis, N.C. State Univ., Raleigh, N.C. 235 p.